GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 15, 2004, 22:31:40 ; Search time 346 Seconds
(without alignments)
4037.027 Million cell updates/sec

Title: US-09-522-753-5
Perfect score: 13215
Sequence: 1 MSGSTQLVAQTWRATEPRYP.....WDEEPKPLLCSQYETLSDSE 2517

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	718	5.4	1922	2	US-08-372-652-9	Sequence 9, Appli
	4	718	5.4	1922	5	PCT-US95-16311-9	Sequence 9, Appli
c	5	689	5.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	6	685	5.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	7	670	5.1	44377	2	US-08-804-227C-7	Sequence 7, Appli
c	8	670	5.1	44377	2	US-08-804-198-1	Sequence 1, Appli
	9	668.5	5.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	10	665	5.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
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c	12	652	4.9	13987	2	US-08-804-227C-13	Sequence 13, Appl
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	16	641	4.9	28958	1	US-08-457-342-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-976-594-306
; Sequence 306, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 306
; LENGTH: 9053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 898877.6
; NAME/KEY: unsure
; LOCATION: 2006, 2012
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-306

Alignment Scores:

Pred. No.:	0	Length:	9053
Score:	12922.00	Matches:	2487
Percent Similarity:	98.26%	Conservative:	2
Best Local Similarity:	98.18%	Mismatches:	10
Query Match:	97.78%	Indels:	35
DB:	4	Gaps:	5

US-09-522-753-5 (1-2517) x US-09-976-594-306 (1-9053)

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Qy        361 LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeuSer 380
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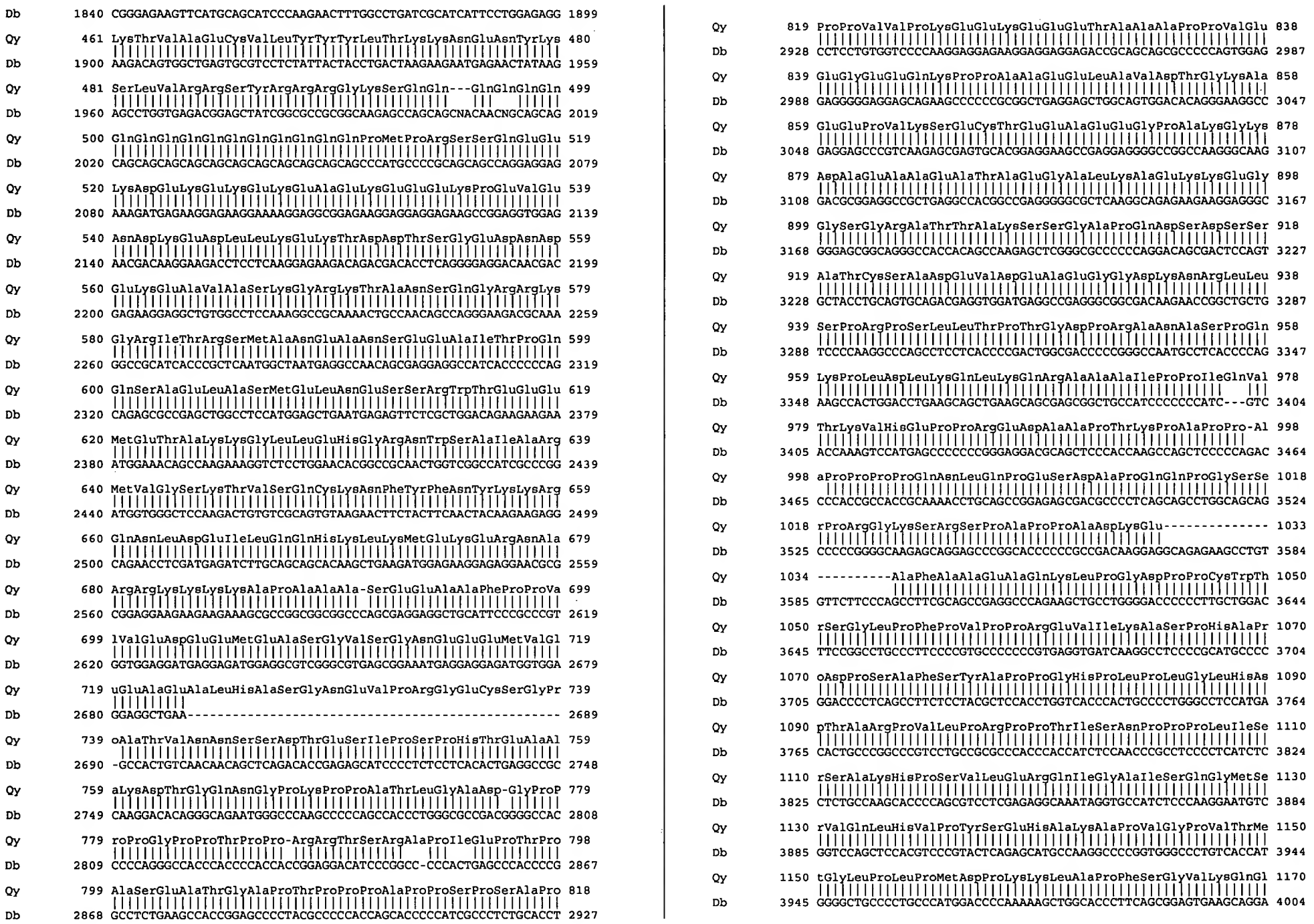
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Db 2749 CAAGGACACAGGGCAGAATGGGCCCAAGCCCCCAGCCACCCTGGGCGCCGACGGGGCCAC 2808
Qy 779 roProGlyProProThrProPro-ArgArgThrSerArgAlaProIleGluProThrPro 798
Db 2809 CCCCAGGGCCACCCACCCCACCACCGGAGGACATCCCGGCC-CCCACTGAGCCCACCCCG 2867
Qy 799 AlaSerGluAlaThrGlyAlaProThrProProProAlaProProSerProSerAlaPro 818
Db 2868 GCCTCTGAAGCCACCGGAGCCCCTACGCCCCCACCAGCACCCCCATCGCCCTCTGCACCT 2927
Qy 819 ProProValValProLysGluGluLysGluGluGluThrAlaAlaAlaProProValGlu 838
Db 2928 CCTCCTGTGGTCCCCAAGGAGGAGAAGGAGGAGGAGACCGCAGCAGCGCCCCCAGTGGAG 2987
Qy 839 GluGlyGluGluGlnLysProProAlaAlaGluGluLeuAlaValAspThrGlyLysAla 858
Db 2988 GAGGGGGAGGAGCAGAAGCCCCCCGCGGCTGAGGAGCTGGCAGTGGACACAGGGAAGGCC 3047
Qy 859 GluGluProValLysSerGluCysThrGluGluAlaGluGluGlyProAlaLysGlyLys 878
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Db 3465 CCCACCGCCACCGCAAAACCTGCAGCCGGAGAGCGACGCCCCTCAGCAGCCTGGCAGCAG 3524
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Qy 1070 oAspProSerAlaPheSerTyrAlaProProGlyHisProLeuProLeuGlyLeuHisAs 1090
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Qy 1150 tGlyLeuProLeuProMetAspProLysLysLeuAlaProPheSerGlyValLysGlnGl 1170
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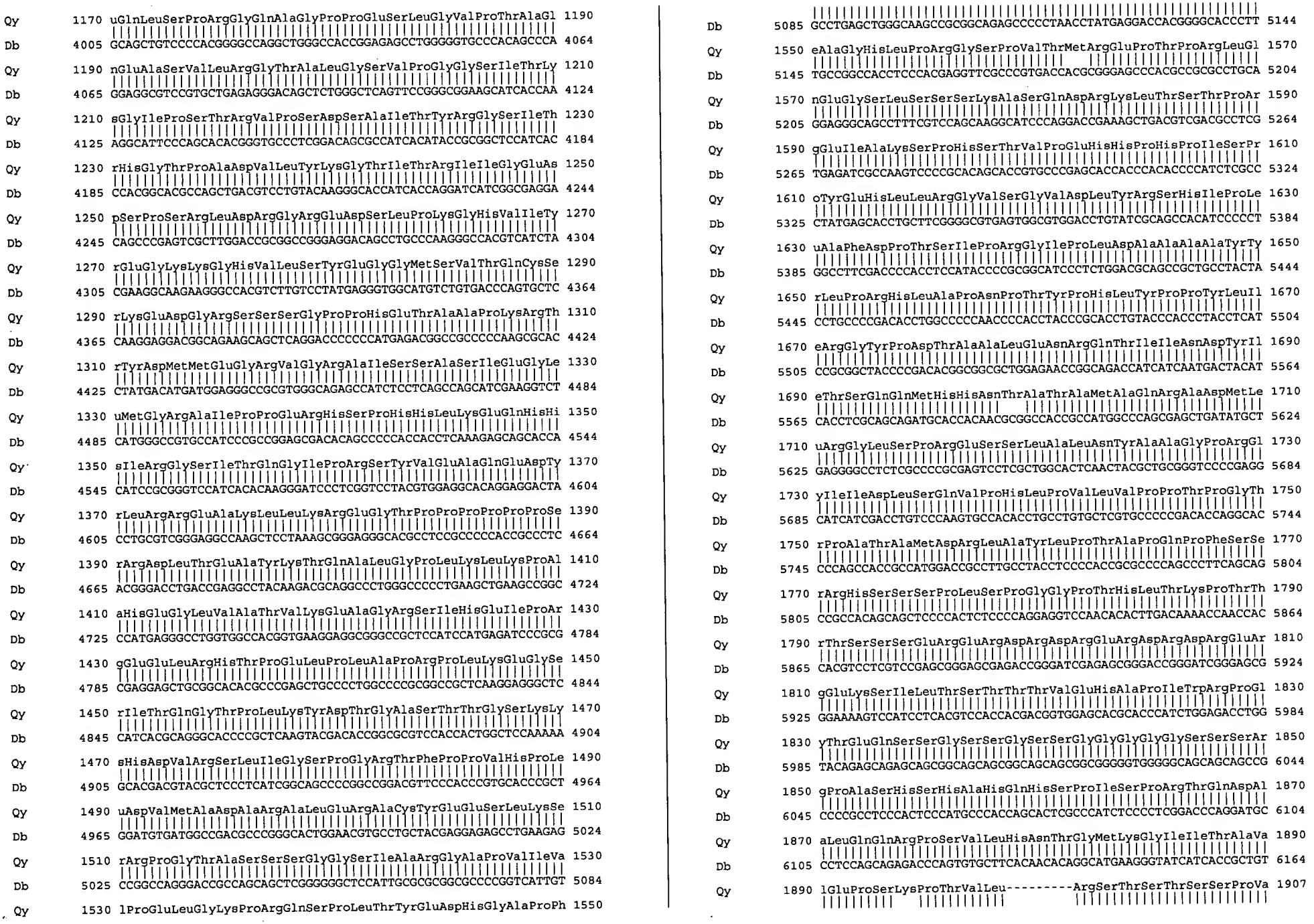
Qy 1170 uGlnLeuSerProArgGlyGlnAlaGlyProProGluSerLeuGlyValProThrAlaGl 1190
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Qy 1190 nGluAlaSerValLeuArgGlyThrAlaLeuGlySerValProGlyGlySerIleThrLy 1210
Db 4065 GGAGGCGTCCGTGCTGAGAGGGACAGCTCTGGGCTCAGTTCCGGGCGGAAGCATCACCAA 4124
Qy 1210 sGlyIleProSerThrArgValProSerAspSerAlaIleThrTyrArgGlySerIleTh 1230
Db 4125 AGGCATTCCCAGCACACGGGTGCCCTCGGACAGCGCCATCACATACCGCGGCTCCATCAC 4184
Qy 1230 rHisGlyThrProAlaAspValLeuTyrLysGlyThrIleThrArgIleIleGlyGluAs 1250
Db 4185 CCACGGCACGCCAGCTGACGTCCTGTACAAGGGCACCATCACCAGGATCATCGGCGAGGA 4244
Qy 1250 pSerProSerArgLeuAspArgGlyArgGluAspSerLeuProLysGlyHisValIleTy 1270
Db 4245 CAGCCCGAGTCGCTTGGACCGCGGCCGGGAGGACAGCCTGCCCAAGGGCCACGTCATCTA 4304
Qy 1270 rGluGlyLysLysGlyHisValLeuSerTyrGluGlyGlyMetSerValThrGlnCysSe 1290
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Qy 1290 rLysGluAspGlyArgSerSerSerGlyProProHisGluThrAlaAlaProLysArgTh 1310
Db 4365 CAAGGAGGACGGCAGAAGCAGCTCAGGACCCCCCCATGAGACGGCCGCCCCCAAGCGCAC 4424
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Qy 1470 sHisAspValArgSerLeuIleGlySerProGlyArgThrProProProValHisProLe 1490
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Qy 1490 uAspValMetAlaAspAlaArgAlaLeuGluArgAlaCysTyrGluGluSerLeuLysSe 1510
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Qy 1630 uAlaPheAspProThrSerIleProArgGlyIleProLeuAspAlaAlaAlaAlaTyrTy 1650
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Qy 1670 eArgGlyTyrProAspThrAlaAlaLeuGluAsnArgGlnThrIleIleAsnAspTyrIl 1690
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Qy       2107 gProLeuProGluSerGlnProSerSerSerProLeuLeuGlnThrAlaProGlyValLy 2127
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Db       7485 TAGAAGCCAGGCGGTGCAGGAACATGCCAGCACCAACATGGGGCTGGAGGCCATAATTAG 7544

Qy       2347 gLysAlaLeuMetGlyLysTyrAspGlnTrpGluGluSerProProLeuSerAlaAsnAl 2367
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Db       7545 AAAGGCACTCATGGGTAAATATGACCAGTGGGAAGAGTCCCCGCCGCTCAGCGCCAATGC 7604

Qy       2367 aPheAsnProLeuAsnAlaSerAlaSerLeuProAlaAlaMetProIleThrAlaAlaAs 2387
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Db       7605 TTTTAACCCTCTGAATGCCAGTGCCAGCCTGCCCGCTGCTATGCCCATAACCGCTGCTGA 7664

Qy       2387 pGlyArgSerAspHisThrLeuThrSerProGlyGlyGlyGlyLysAlaLysValSerGl 2407
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Db       7665 CGGACGGAGTGACCACACACTCACCTCGCCAGGTGGCGGCGGGAAGGCCAAGGTCTCTGG 7724

Qy       2407 yArgProSerSerArgLysAlaLysSerProAlaProGlyLeuAlaSerGlyAspArgPr 2427
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Qy       2427 oProSerValSerSerValHisSerGluGlyAspCysAsnArgArgThrProLeuThrAs 2447
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Db       7785 ACCCTCTGTCTCCTCAGTGCACTCGGAGGGAGACTGCAACCGCCGGACGCCGCTCACCAA 7844

Qy       2447 nArgValTrpGluAspArgProSerSerAlaGlySerThrProPheProTyrAsnProLe 2467
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Db       7845 CCGCGTGTGGGAGGACAGGCCCTCGTCCGCAGGTTCCACGCCATTCCCCTACAACCCCCT 7904

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Qy       2487 ySerGlyProLeuAlaGlyProHisHisAlaTrpAspGluGluProLysProLeuLeuCy 2507
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Qy       2507 sSerGlnTyrGluThrLeuSerAspSerGlu 2517
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Db       8025 CTCGCAGTACGAGACACTCTCCGACAGCGAG 8055

RESULT 2
US-09-144-085-3/c
; Sequence 3, Application US/09144085
; Patent No. 6280999
; GENERAL INFORMATION:
;  APPLICANT: Gustafsson, Claes
;  APPLICANT: Betlach, Mary C.
;  APPLICANT: Ashley, Gary
;  APPLICANT: Julien, Bryan
;  APPLICANT: Ziermann, Rainer
;  TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
;  TITLE OF INVENTION: THEREFOR
;  FILE REFERENCE: 30062-20020.20
;  CURRENT APPLICATION NUMBER: US/09/144,085
;  CURRENT FILING DATE: 1998-08-31
;  EARLIER APPLICATION NUMBER: 09/010,809
;  EARLIER FILING DATE: 1998-01-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
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;   LENGTH: 33529
;   TYPE: DNA
;   ORGANISM: Sorangium cellulosum
US-09-144-085-3

Alignment Scores:
Pred. No.:                7.28e-21      Length:          33529
Score:                    726.50        Matches:         674
Percent Similarity:       32.36%        Conservative:    314
Best Local Similarity:    22.08%        Mismatches:      1199
Query Match:              5.50%         Indels:          873
DB:                       3             Gaps:            137

US-09-522-753-5 (1-2517) x US-09-144-085-3 (1-33529)

Qy        17 ProArgTyrProPro---HisSerLeuSerTyrProValGlnIleAlaArgThrHisThr 35
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Db     22056 CTGCGCATTCACCGCGGCCTCGTCTCGACCCGACAGCACCAGCGGCAATAGCGCAGGCGC 21997

Qy       238 AlaGluAlaAlaHisArgIleLeuGluGlyLeuGly------------------------ 249
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Qy       249 ------------------------------------------------------------ 249
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Qy       269 AsnIleLysIleAsn-----------GlnAlaMetArgLysLysLeuIleLeuTyrPhe 284
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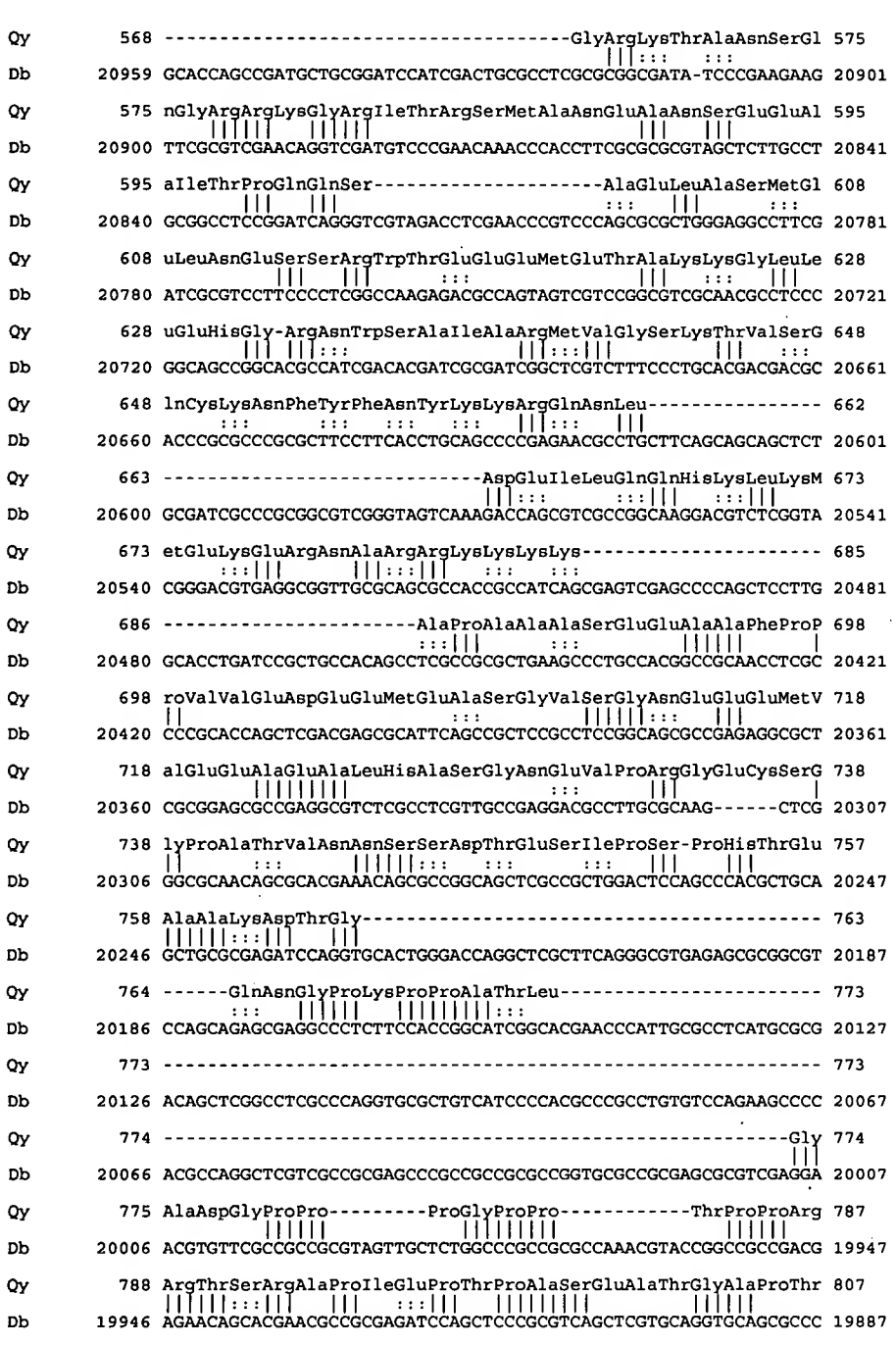
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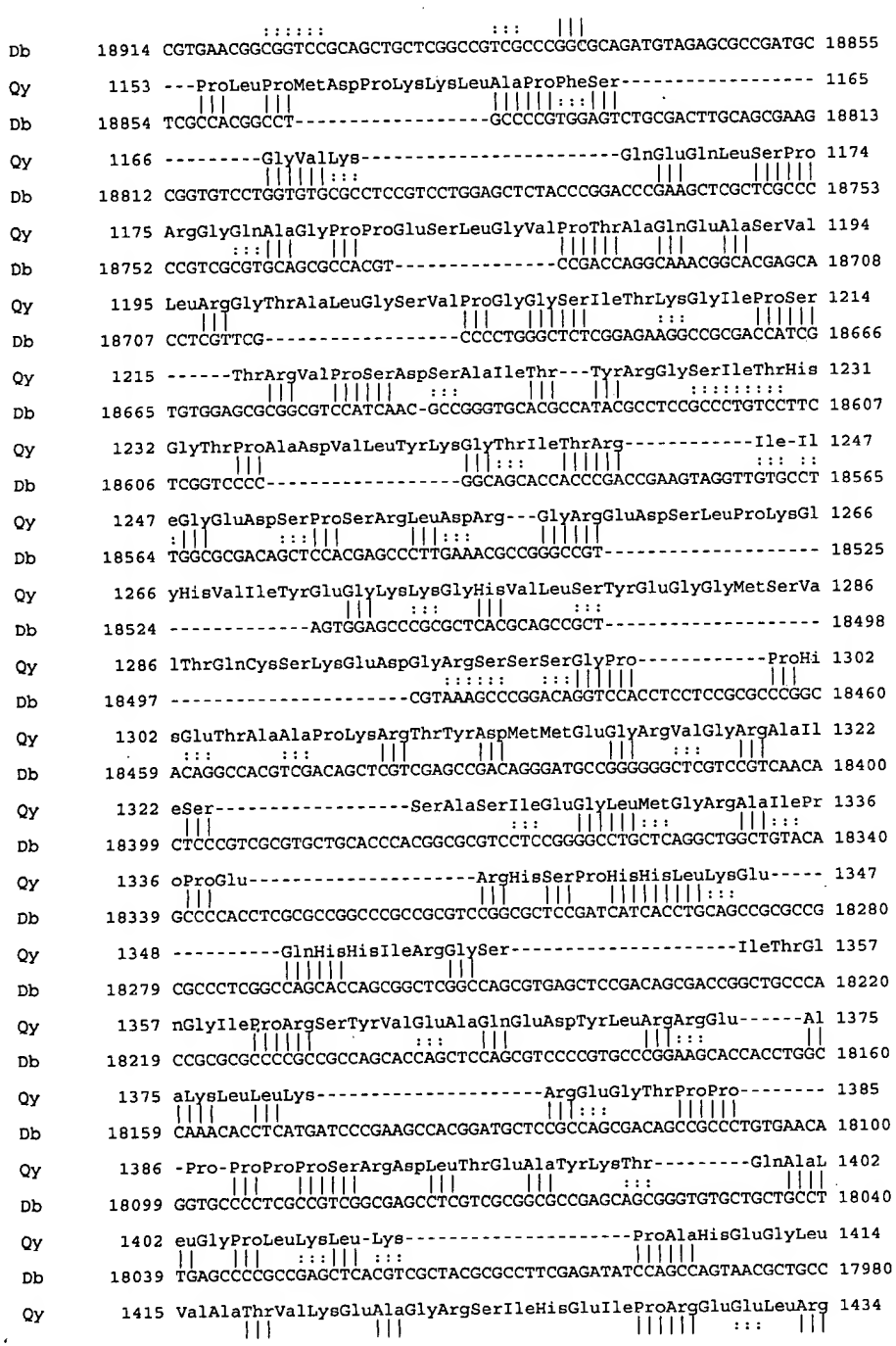
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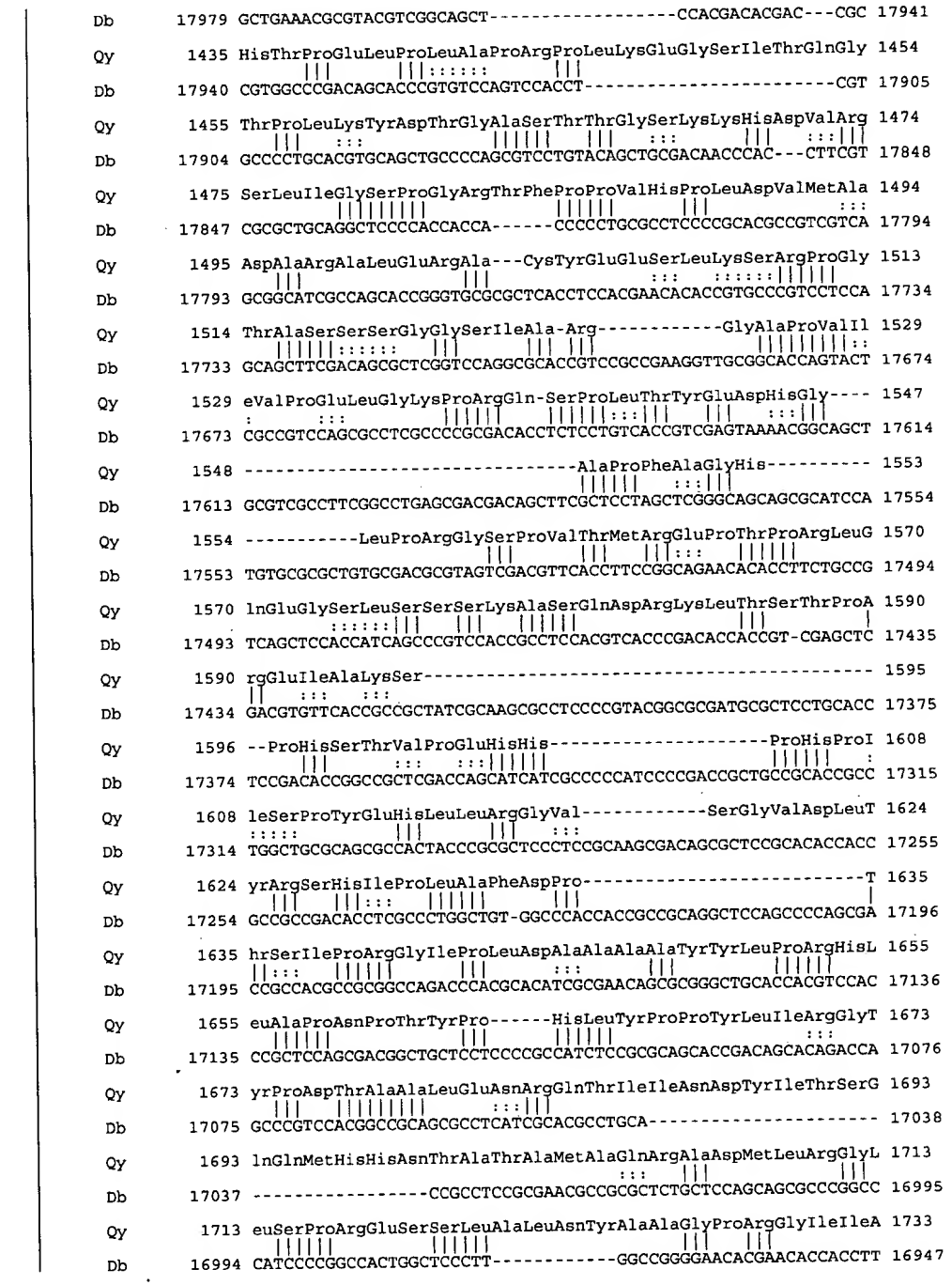
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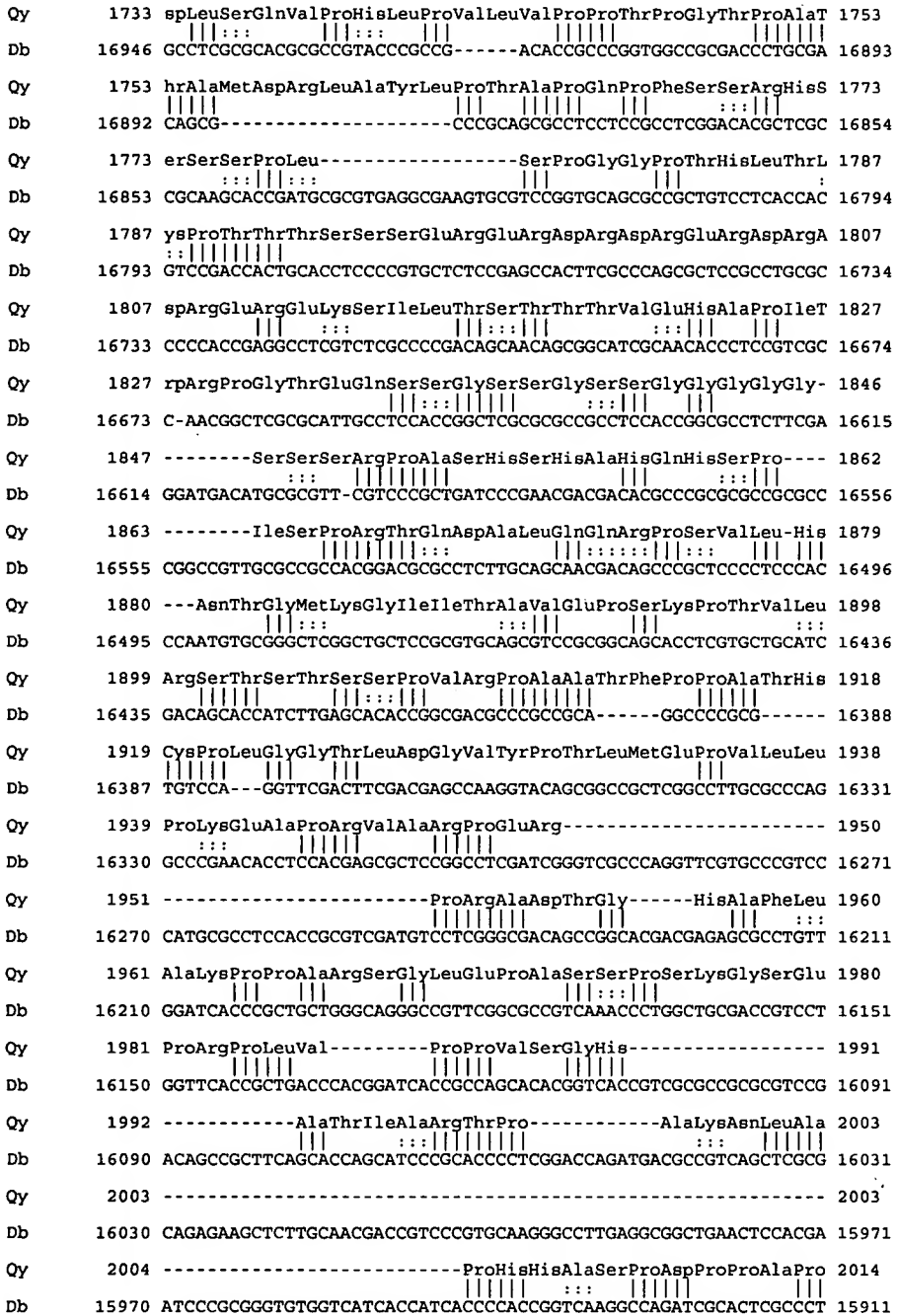
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Db 16330 GCCCGAACACCTCCACGAGCGCTCCGGCCTCGATCGGGTCGCCCAGGTTCGTGCCCGTCC 16271
Qy 1951 ------------------------ProArgAlaAspThrGly------HisAlaPheLeu 1960
Db 16270 CATGCGCCTCCACCGCGTCGATGTCCTCGGGCGACAGCCGGCACGACGAGAGCGCCTGTT 16211
Qy 1961 AlaLysProProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGlu 1980
Db 16210 GGATCACCCGCTGCTGGGCAGGGCCGTTCGGCGCCGTCAAACCCTGGCTGCGACCGTCCT 16151
Qy 1981 ProArgProLeuVal---------ProProValSerGlyHis------------------ 1991
Db 16150 GGTTCACCGCTGACCCACGGATCACCGCCAGCACACGGTCACCGTCGCGCCGCGCGTCCG 16091
Qy 1992 ------------AlaThrIleAlaArgThrPro------------AlaLysAsnLeuAla 2003
Db 16090 ACAGCCGCTTCAGCACCAGCATCCCGCACCCCTCGGACCAGATGACGCCGTCAGCTCGCG 16031
Qy 2003 -- 2003
Db 16030 CAGAGAAGCTCTTGCAACGACCGTCCCGTGCAAGGGCCTTGAGGCGGCTGAACTCCACGA 15971
Qy 2004 -------------------------ProHisHisAlaSerProAspProProAlaPro 2014
Db 15970 ATCCCGCGGGTGTGGTCATCACCATCACCCCACCGGTCAAGGCCAGATCGCACTCGCCCT 15911
Qy 2015 ProAla--------------SerAlaSerAspProHisArgGluLysThrGlnSerLys 2029
Db 15910 GACGCAGGGCCGTGCACGCCAGGTGCAGCGACACCAGCGACGACGAGCACGCCGTGTCCA 15851
Qy 2030 ProPheSerIleGlnGluLeuGluLeuArgSerLeuGlyTyrHisGlySerSerTyrSer 2049
Db 15850 CCG-----------------------TGATCGCTGGGCCCTGCAGCCCGAGCACGTACG 15815
Qy 2050 ProGluGlyValGluProValSerProValSer---SerProSerLeuThrHisAspLys 2068
Db 15814 CCACACGGCCTGAGAGCACGCTCGCCGCGCTCCCGGTGCCCCGGT--------------- 15770
Qy 2069 GlyLeuProLysHisLeuGluGluLeuAspLysSerHisLeuGluGlyGluLeuArgPro 2088
Db 15769 AGCCGTCCAACGCCGCCAGGTCGCTGCCGTAAAGAGCACCGTAGTCCGAGC------CCA 15716
Qy 2089 LysGlnProGlyProValLysLeuGlyGlyGluAlaAlaHisLeuProHisLeuArgPro 2108
Db 15715 TCGAGCCCAGGTACACCCCGGTGGAGCTCTCGCTCAGCGCCGACGGGCGCACGCCAGCCC 15656
Qy 2109 LeuProGluSerGlnProSerSerSerProLeuLeuGlnThrAlaProGlyValLysGly 2128
Db 15655 GCTCCA---GTGCCTCCCACGCCGTCTCCA-----------GCACCAGCCGCTGCTGGG 15611
Qy 2129 HisGlnArgValValThrLeuAlaGlnHisIleSerGluValIleThrGlnAspTyrThr 2148
Db 15610 GATCCATCGCCTGCGCCTCTCGGGGCG-------------------------ATATCC 15578
Qy 2149 ArgHisHisProGlnGlnLeuSerAlaProLeuProAlaProLeuTyrSerPheProGly 2168
Db 15577 CGAAGAAACCCGCATCGA---ACAGGTCGATGTCCCGCAGGAATCCACCCTCGCGCACGT 15521
Qy 2169 AlaSerCysProValLeuAspLeuArgArgProProSerAspLeuTyrLeuProProPro 2188
Db 15520 AGGTCTTGCCCA-----------------------------------CCGCCTCCG 15500
Qy 2189 AspHisGlyAlaProAlaArgGlySerProHisSerGluGlyGlyLysArg--------- 2205
Db 15499 GATCGGGGTCGTAAATCGAAGGTGCATCCCAGCGCGCAGGGAAGGCCTCGATCGCATCTC 15440
Qy 2206 SerProGluProAsnLysThrSer---------------------------------- 2213
Db 15439 TCCCCTCCTCCAGGAGACGCCAGTAGTCTTCCGGCGTAGCGACGCCCCCCGGCAGCCGGC 15380
Qy 2214 ------------------------ValLeuGlyGlyGlyGluAspGlyIleGluProVal 2225
Db 15379 ACGCCATCGATACGATGGCGATGGGCCCTGAACGGAGATCCGAGTGGCTGGCCTGCAGCC 15320
Qy 2226 SerProProGluGlyMet------ThrGluProGlyHisSer------------------ 2237
Db 15319 TCTGCAACTCTTTCAATGCACGGGTCAACGCCTCACGAAGCGTAGGAGAGGCGGCGCTGC 15260
Qy 2238 ---------ArgSerAlaValTyrProLeuLeuTyrArg-----------------Asp 2248
Db 15259 TATTCATGGAGATCCTCTGAGTTCGAAATCATTTGCAAGGCTTGCAAGGCCAGCTGCTCG 15200
Qy 2249 GlyGluGlnThrGluProSerArgMetGlySer--------------------------- 2259
Db 15199 TCGGCGAGATCTTCGAAATCGGAAATGGGAACCGGAACCTCGACGGATGTTTCGGACGGC 15140
Qy 2260 ---LysSerProGlyAsnThrSerGlnProProAlaPhePheSerLysLeuThrGluSer 2278
Db 15139 CCCCGCAGCTCCAAGAGCTTGGGGAGGAGGCCTGAACGACGCACGAGACTGACGGAGAGG 15080
Qy 2279 AsnSerAlaMetValLysSerLysLysGlnGluIleAsnLysLysLeuAsnThrHisAsn 2298
Db 15079 CTGAGCATGAACGCGCGAATTTCCTCGTCGGACATGGAGTCCGCTGTACGCAGCAGATTC 15020
Qy 2299 ArgAsnGluProGluTyrAsnIleSerGlnProGlyThrGluIlePheAsnMetProAla 2318
Db 15019 CGGCGCTCACCGTTTCCGAACTTTGACAGGAGGAAC---------TTCGCGATGTGCGTG 14969
Qy 2319 IleThrGly-----------------ThrGlyLeuMetThrTyrArgSerGlnAlaVal 2332

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Db      14968 GCAGATGGATGGTCGAAAAGCAAAGTGGCAGGCAAGTTGCTTCCGACCAGCAAGGCGAGC 14909

Qy       2333 GlnGluHisAlaSerThrAsnMetGlyLeuGluAlaIleIleArgLysAlaLeuMetGly 2352

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Db      14884 --------------AGCGAATCCATTCCGAGCTCCCTCAAGGGCTGGGCCGTAGGAATC 14840

Qy       2373 AlaSerAlaSerLeuProAlaAlaMetProIleThrAlaAlaAspGlyArgSerAspHis 2392

Db      14839 GCGTCA---------CCGCGCTGAAGCCCGAGCACCGCGGCGACCTCGGCCCGCACAAGG 14789

Qy       2393 ThrLeuThrSerProGlyGlyGlyGlyLysAlaLysValSerGlyArgProSerSerArg 2412

Db      14788 TCGATGAGCGAGCTC-----------AGGCGCTCCGCCTCCGGCAGCGCCGAGAGGCGC 14741

Qy       2413 LysAlaLysSerProAlaProGlyLeuAlaSerGlyAsp------ArgProProSerVal 2430

Db      14740 TCGCGGAGCGTCGACGCCTCCTTCCTCGCGGCAGAGGACGCCTTGCGCAGCCCGGGGCGC 14681

Qy       2431 SerSerValHisSerGluGly--------------------------------AspCys 2439

Db      14680 ACCAGCGCGCGAAGCAGCGCCGGCAGCTCGCCGCTGGACTCCAGCCCACGCTGCAGCTGC 14621

Qy       2440 AsnArgArgThrProLeuThrAsnArgValTrpGluAspArgProSerSerAlaGlySer 2459

Db      14620 GCGAGATCCAGGTGCACTGGGACCAGGCTCGCTTCAGAGCGTGAGAGCGCGGCGTCCAGC 14561

Qy       2460 ThrProPheProTyrAsn-ProLeu------------------------------IleMe 2469

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Qy       2469 tArgLeuGlnAlaGlyValMetAlaSerProProPro------ProGlyLeuProAla-- 2486

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Qy       2487 -GlySerGlyProLeuAla 2492

Db      14440 AGGCTCGTCGCCGCGAGCC 14422
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RESULT 3
US-08-372-652-9
; Sequence 9, Application US/08372652
; Patent No. 5932699
;  GENERAL INFORMATION:
;    APPLICANT:  Moore, David
;    APPLICANT:  Seol, Wongi
;    APPLICANT:  Choi, Hueng-Sik
;    TITLE OF INVENTION:  RETINOID X RECEPTOR-INTERACTING
;    TITLE OF INVENTION:  POLYPEPTIDES AND RELATED MOLECULES AND METHODS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street, Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/372,652
;      FILING DATE:  13-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/246001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1922 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-372-652-9

Alignment Scores:
Pred. No.:                9.5e-22        Length:          1922
Score:                    718.00         Matches:         212
Percent Similarity:       48.81%         Conservative:    76
Best Local Similarity:    35.93%         Mismatches:      214
Query Match:              5.43%          Indels:          88
DB:                       2              Gaps:            25

US-09-522-753-5 (1-2517) x US-08-372-652-9 (1-1922)

Qy       1975 ProSerLysGlySerGluProArgProLeuVal--------------------------- 1985

Db        209 CCAAGTGGCAAGGCCCAGCCTCATGCCTCAGTAGTGTATTCTGAGGCTGGGAAAGATAAA 268

Qy       1986 ------ProProValSerGlyHisAlaThrIleAlaArgThrProAlaLysAsn------ 2001

Db        269 GGGCCTCCTCCAAAATCCAGATATGAGGAAGAGCTAAGGACCCGAGGGAAGACTACCATT 328

Qy       2002 LeuAlaProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAspPro 2021

Db        329 ACTGCAGCTAACTTCATAGACGTGACCATCACCCGGCAAATTGCCTCGGACAAGGATGCG 388

Qy       2022 HisArgGluLysThrGlnSerLysProPheSerIleGlnGluLeuGluLeuArgSerLeu 2041

Db        389 AGGGAACGTGGCTCTCAAAGTTCAGACTCTTCT-----------------AGTAGCTTG 430

Qy       2042 GlyTyrHisGlySerSerTyrSerProGluGlyValGluProValSerProValSerSer 2061

Db        431 TCTTCTCACAGGTATGAAACGGCTAGTGATGCCATTGAGGTGATAAGTCCCGCCAGCTCA 490

Qy       2062 ProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluGluLeuAspLysSerHis 2081

Db        491 CCTGCACCACCCCAGGAAAAGCCACAGGCCTATCAGCCAGACATGGTTAAGGCAAATCAA 550

Qy       2082 LeuGluGlyGluLeuArgProLysGlnProGlyProValLysLeuGlyGlyGluAlaAla 2101

Db        551 GCAGAAAATGAGTCCACTCGACAGTATGAAGGTCCA----------------------- 586

Qy       2102 HisLeuProHisLeuArg--------------ProLeuProGluSerGlnProSerSer 2116

Db        587 ---CTGCATCATTATCGGTCCCAGCAGGAATCACCATCTCCACAGCAACAGCCACCACTG 643

Qy       2117 SerProLeuLeuGlnThr------AlaProGlyValLysGlyHisGlnArgValValThr 2134

Db        644 CCCCCATCTTCCCAGTCAGAGGGAATGGGACAGGTGCCCAGGACCCATCGACTGATCACA 703

Qy       2135 LeuAlaGlnHisIleSerGluValIleThrGlnAspTyrThrArgHisHisProGlnGln 2154

Db        704 CTTGCTGACCACATCTGTCAAATTATCACACAAGATTTTGCTAGAAAT------CAAGTT 757

Qy       2155 LeuSerAlaProLeuProAlaProLeuTyrSerPheProGlyAla------SerCysPro 2172

Db        758 CCCTCGCAGCCTTCTACTTCTACATTCCAAACTTCACCATCTGCTTTGTCATCCACACCT 817

Qy       2173 ValLeuAspLeuArgArgProProSerAspLeuTyrLeuProProProAsp--------- 2189

Db        818 GTA---------AGAACTAAAACCTCAAGCCGCTACAGCCCAGAATCACAGTCTCAGACT 868

Qy       2190 ------HisGlyAlaProAla---ArgGlySerProHis---------------SerGlu 2201
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Db        869 GTCTTGCATCCCAGACCAGGTCCTAGAGTCTCTCCAGAAAATCTTGTGGATAAATCCCGG 928

Qy       2202 GlyGlyLysArgSerProGluProAsnLysThrSerValLeuGlyGlyGlyGluAspGly 2221

Db        929 GGAAGCAGGCCTGGAAAATCTCCAGAGAGGAGTCATATC---------CCATCAGAGCCC 979

Qy       2222 IleGluProValSerProProGluGlyMetThrGluProGlyHisSerArgSerAlaVal 2241

Db        980 TATGAGCCCATCTCCCCACCCCAAGGCCCTGCTGTG------CATGAGAAGCAGGACAGC 1033

Qy       2242 TyrProLeuLeuTyrArgAspGlyGluGlnThrGluProSerArgMetGlySerLysSer 2261

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Qy       2262 ProGlyAsnThrSerGlnProProAlaPhePheSerLysLeuThrGluSerAsnSerAla 2281

Db       1094 CCAGGAAGTATAAGCTACTTGCCTTCATTCTTCACCAAGCTT---GAAAGCACATCACCC 1150

Qy       2282 MetValLysSerLysLysGlnGluIleAsnLysLysLeuAsnThrHisAsnArgAsnGlu 2301

Db       1151 ATGGTTAAATCAAAGAAACAGGAAATTTTTCGTAAGTTGAACTCTTCTGGTGGAGGTGAC 1210

Qy       2302 ProGluTyrAsnIleSerGlnProGlyThrGluIlePheAsnMetProAlaIleThrGly 2321

Db       1211 TCTGATATGGCAGCTGCTCAGCCAGGAACAGAGATCTTCAATCTGCCAGCAGTTACCACA 1270

Qy       2322 ThrGlyLeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMetGly 2341

Db       1271 TCAGGTGCAGTGAGCTCAAGAAGCCATTCTTTTGCTGATCCCGCCAGT---AACCTTGGT 1327

Qy       2342 LeuGluAlaIleIleArgLysAlaLeuMetGlyLysTyrAspGlnTrpGluGlu------ 2359

Db       1328 CTAGAAGACATCATCAGAAAGGCTCTCATGGGAAGTTTTGATGATAAAGTTGAAGATCAT 1387

Qy       2360 ------------SerProProLeuSerAlaAsnAlaPheAsnProLeuAsnAlaSerAla 2375

Db       1388 GGTGTTGTCATGTCCCATCCTGTG---------GGCATTATGCCTGGTAGTGCCAGCACC 1438

Qy       2376 SerLeuProAlaAlaMetProIleThrAlaAlaAspGlyArgSerAspHisThrLeuThr 2395

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Qy       2396 SerProGlyGlyGly---GlyLysAlaLysValSerGlyArgProSerSerArgLysAla 2414

Db       1484 TCACCTCATGCAGGAGTATGCAAACCAAAGCTGATCAACAAATCAAACAGCAGGAAGTCT 1543

Qy       2415 LysSerProAlaProGlyLeuAla------SerGlyAspArgProProSerValSerSer 2432

Db       1544 AAATCTCCTATTCCTGGGCAAAGCTATTTAGGAACTGAAAGGCCTTCTTCTGTCTCCTCT 1603

Qy       2433 ValHisSerGluGlyAspCysAsnArgArgThrProLeuThrAsnArgValTrpGluAsp 2452

Db       1604 GTGCATTCAGAAGGTGATTACCACAGGCAGACACCA------GGATGGGCATGGGAAGAT 1657

Qy       2453 ArgProSerSerAlaGlySerThrProPheProTyrAsnProLeuIleMetArgLeuGln 2472

Db       1658 CGGCCCTCTTCAACAGGTTCTACTCAGTTCCCTTACAACCCTCTGACCATACGGATG--- 1714

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Db       1715 ---------CTCAGCAGTACACCACCTACACAGATCGCATGCGCCCCATCTGCCATCACC 1765

Qy       2492 ---AlaGlyProHis---------HisAlaTrpAspGluGluProLysProLeuLeuCys 2507

Db       1766 CAAGCAGCTCCACATCAACAGAACCGCATCTGGGAGAGGGAGCCTGCCCCGCTCCTCTCA 1825

Qy       2508 SerGlnTyrGluThrLeuSerAspSerGlu 2517

Db       1826 GCGCAGTATGAGACACTGTCTGATAGTGAC 1855

RESULT 4
PCT-US95-16311-9
; Sequence 9, Application PC/TUS9516311
;  GENERAL INFORMATION:
;    APPLICANT:  Moore, David
;    APPLICANT:  Seol, Wongi
;    APPLICANT:  Choi, Hueng-Sik
;    TITLE OF INVENTION:  RETINOID X RECEPTOR-INTERACTING
;    TITLE OF INVENTION:  POLYPEPTIDES AND RELATED MOLECULES AND METHODS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street, Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/16311
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/372,652
;      FILING DATE:  13-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/246001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1922 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-16311-9

Alignment Scores:
Pred. No.:              9.5e-22         Length:         1922
Score:                  718.00          Matches:        212
Percent Similarity:     48.81%          Conservative:   76
Best Local Similarity:  35.93%          Mismatches:     214
Query Match:            5.43%           Indels:         88
DB:                     5               Gaps:           25

US-09-522-753-5 (1-2517) x PCT-US95-16311-9 (1-1922)

Qy       1975 ProSerLysGlySerGluProArgProLeuVal-------------------------- 1985

Db        209 CCAAGTGGCAAGGCCCAGCCTCATGCCTCAGTAGTGTATTCTGAGGCTGGGAAAGATAAA 268

Qy       1986 ------ProProValSerGlyHisAlaThrIleAlaArgThrProAlaLysAsn------ 2001

Db        269 GGGCCTCCTCCAAAATCCAGATATGAGGAAGAGCTAAGGACCCGAGGGAAGACTACCATT 328

Qy       2002 LeuAlaProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAspPro 2021

Db        329 ACTGCAGCTAACTTCATAGACGTGACCATCACCCGGCAAATTGCCTCGGACAAGGATGCG 388

Qy       2022 HisArgGluLysThrGlnSerLysProPheSerIleGlnGluLeuGluLeuArgSerLeu 2041

Db        389 AGGGAACGTGGCTCTCAAAGTTCAGACTCTTCT----------------AGTAGCTTG 430

Qy       2042 GlyTyrHisGlySerSerTyrSerProGluGlyValGluProValSerProValSerSer 2061

Db        431 TCTTCTCACAGGTATGAAACGGCTAGTGATGCCATTGAGGTGATAAGTCCCGCCAGCTCA 490

Qy       2062 ProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluGluLeuAspLysSerHis 2081
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Db        491 CCTGCACCACCCCAGGAAAAGCCACAGGCCTATCAGCCAGACATGGTTAAGGCAAATCAA 550

Qy       2082 LeuGluGlyGluLeuArgProLysGlnProGlyProValLysLeuGlyGlyGluAlaAla 2101

Db        551 GCAGAAAATGAGTCCACTCGACAGTATGAAGGTCCA---------------------------- 586

Qy       2102 HisLeuProHisLeuArg---------------ProLeuProGluSerGlnProSerSer 2116

Db        587 ---CTGCATCATTATCGGTCCCAGCAGGAATCACCATCTCCACAGCAACAGCCACCACTG 643

Qy       2117 SerProLeuLeuGlnThr------AlaProGlyValLysGlyHisGlnArgValValThr 2134

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Qy       2135 LeuAlaGlnHisIleSerGluValIleThrGlnAspTyrThrArgHisHisProGlnGln 2154

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Db        758 CCCTCGCAGCCTTCTACTTCTACATTCCAAACTTCACCATCTGCTTTGTCATCCACACCT 817

Qy       2173 ValLeuAspLeuArgArgProProSerAspLeuTyrLeuProProProAsp--------- 2189

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Qy       2190 ------HisGlyAlaProAla---ArgGlySerProHis--------------SerGlu 2201

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Qy       2242 TyrProLeuLeuTyrArgAspGlyGluGlnThrGluProSerArgMetGlySerLysSer 2261

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Qy       2262 ProGlyAsnThrSerGlnProProAlaPhePheSerLysLeuThrGluSerAsnSerAla 2281

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Qy       2302 ProGluTyrAsnIleSerGlnProGlyThrGluIlePheAsnMetProAlaIleThrGly 2321

Db       1211 TCTGATATGGCAGCTGCTCAGCCAGGAACAGAGATCTTCAATCTGCCAGCAGTTACCACA 1270

Qy       2322 ThrGlyLeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMetGly 2341

Db       1271 TCAGGTGCAGTGAGCTCAAGAAGCCATTCTTTTGCTGATCCCGCCAGT---AACCTTGGT 1327

Qy       2342 LeuGluAlaIleIleArgLysAlaLeuMetGlyLysTyrAspGlnTrpGluGlu------ 2359

Db       1328 CTAGAAGACATCATCAGAAAGGCTCTCATGGGAAGTTTTGATGATAAAGTTGAAGATCAT 1387

Qy       2360 -----------SerProProLeuSerAlaAsnAlaPheAsnProLeuAsnAlaSerAla 2375

Db       1388 GGTGTTGTCATGTCCCATCCTGTG---------GGCATTATGCCTGGTAGTGCCAGCACC 1438

Qy       2376 SerLeuProAlaAlaMetProIleThrAlaAlaAspGlyArgSerAspHisThrLeuThr 2395

Db       1439 TCAGTG--------------GTGACGAGCAGCGAGGCACGGAGAGATGAAGGGGAGCCA 1483

Qy       2396 SerProGlyGlyGly---GlyLysAlaLysValSerGlyArgProSerSerArgLysAla 2414

Db       1484 TCACCTCATGCAGGAGTATGCAAACCAAAGCTGATCAACAAATCAAACAGCAGGAAGTCT 1543

Qy       2415 LysSerProAlaProGlyLeuAla------SerGlyAspArgProProSerValSerSer 2432

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Db       1715 ---------CTCAGCAGTACACCACCTACACAGATCGCATGCGCCCCATCTGCCATCACC 1765

Qy       2492 ---AlaGlyProHis---------HisAlaTrpAspGluGluProLysProLeuLeuCys 2507

Db       1766 CAAGCAGCTCCACATCAACAGAACCGCATCTGGGAGAGGGAGCCTGCCCCGCTCCTCTCA 1825

Qy       2508 SerGlnTyrGluThrLeuSerAspSerGlu 2517

Db       1826 GCGCAGTATGAGACACTGTCTGATAGTGAC 1855
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RESULT 5
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:

Pred. No.:	3.28e-17	Length:	4411529
Score:	689.00	Matches:	526
Percent Similarity:	33.44%	Conservative:	207
Best Local Similarity:	24.00%	Mismatches:	872
Query Match:	5.21%	Indels:	599
DB:	3	Gaps:	91

US-09-522-753-5 (1-2517) x US-09-103-840A-1 (1-4411529)

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Qy        546 LeuLysGluLysThrAspAspThrSerGlyGluAspAsnAspGluLysGluAlaValAla 565

Db     841474 GTTCGTCGGAAGGTGATGGGGCTGGGCGGTGACGGCTTCGACGAATGCGAATGCCTCTGC 841415

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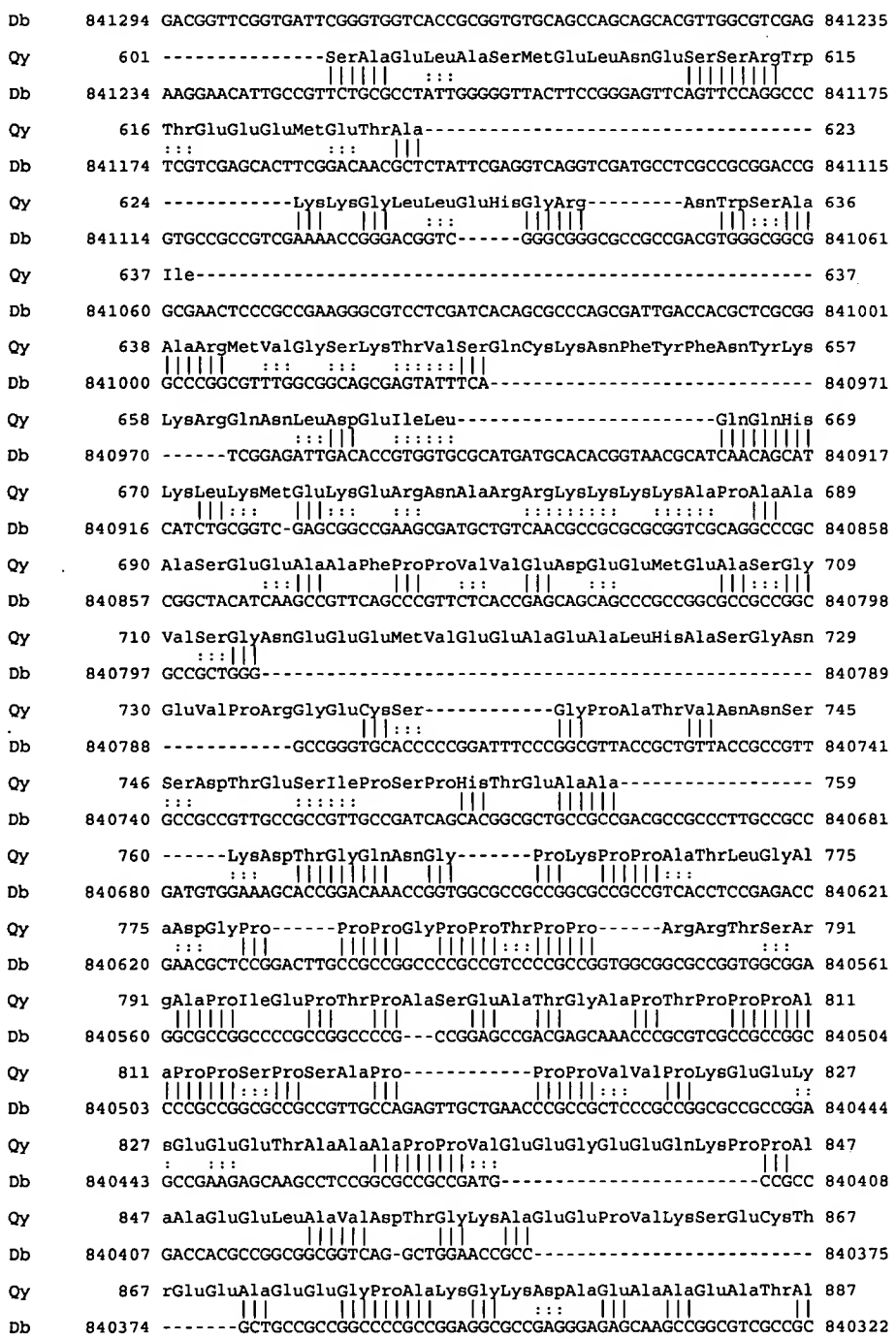
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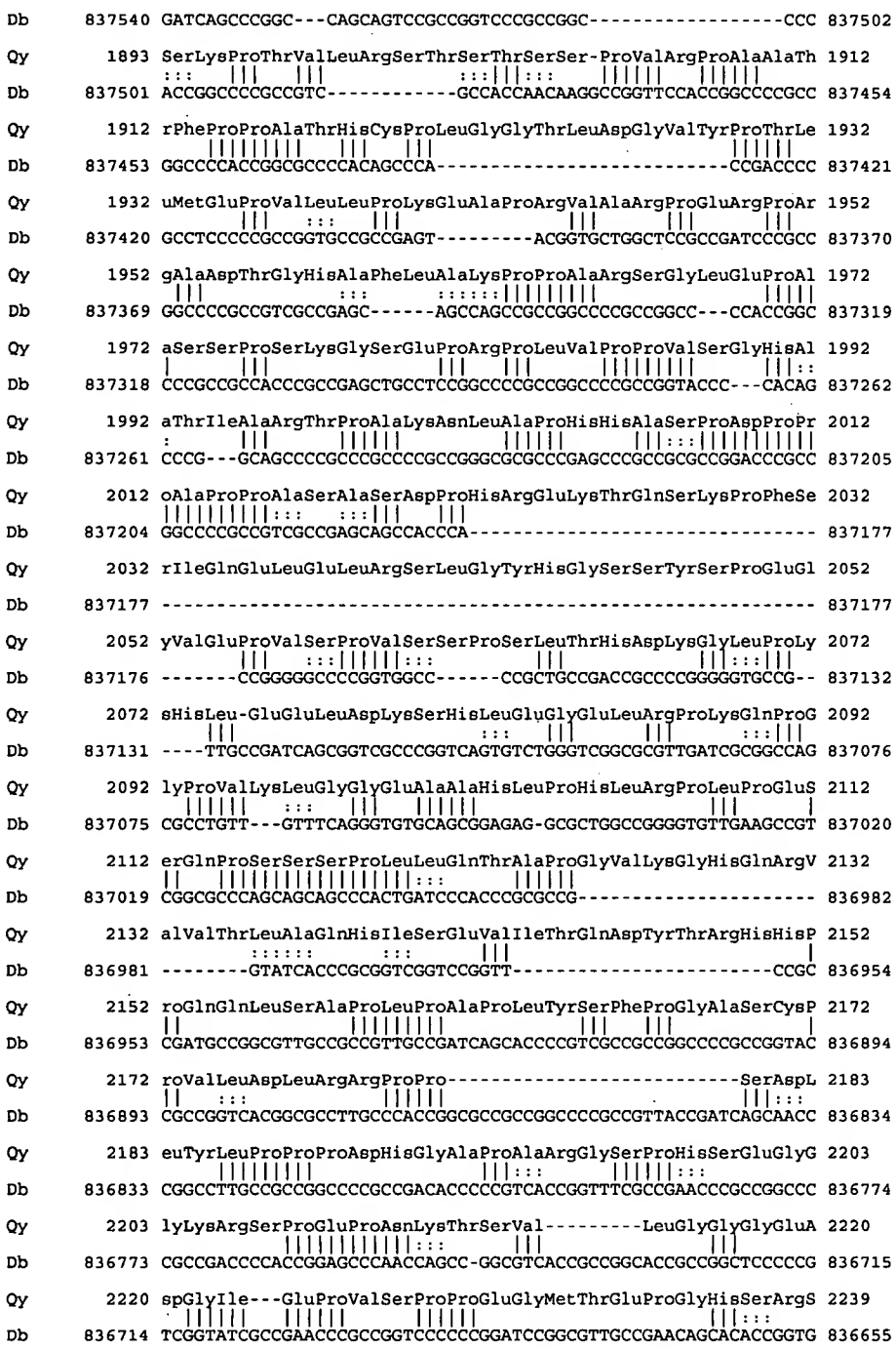
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